

Please replace the paragraph beginning at **page 25, line 18**, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

*S.aureus* pdf has seven insertions with respect to the *E.coli* sequence (Figure 10). The first insertion T3-M4 adds some additional hydrophobic surface area which forms a small surface for interaction with the third insertion (the extended n-terminal helix) N43-G54. The insertion after P25 adds one additional residue to the turn, which leads into the first long helix of pdf. This n-terminal helix is extended by an additional helix (insertion three N43-G54) which is not present in the *E.coli* structure. In the *E.coli* structure this helix is followed by a beta turn which drops down into the very conserved GXGLAA (SEQ ID NO:9) sequence which forms the third (and edge) strand of the n-terminal  $\beta$ -sheet. This strand also forms part of the wall of the active site crevice and provides loci for hydrogen bonding of peptide substrates (Hao et al., *Biochemistry*, 38: 4712-19 (1999)). The insertion of residues G81-G83 in the *S.aureus* structure extends the turn between strands II and III of the n-terminal  $\beta$ -sheet. The insertion of V100 is in the turn between strand I of the central anti-parallel  $\beta$ -sheet and the central strand of the c-terminal mixed sheet. Insertion six occurs at the end of the central strand of the mix sheet and includes P106 and T107. These residues are positioned at the opening of the active site crevice and may be important determinates of *S.aureus* specificity. The subsequent conserved residues EGCLS (SEQ ID NO:10) form the other wall of the active site crevice. Residue C111 at the center of this sequence is one of the active site metal ligands. The conserved glutamic acid projects downward to form a part of the crevice wall and makes a conserved salt bridge with R124, which is found in the center of the first strand of the mix  $\beta$ -sheet. The insertion of A119 results in a slight bulge of the connecting strand (with respect to the *E.coli* structure) which precedes the first strand of the c-terminal mixed  $\beta$ -sheet. This seventh insertion, the sixth insertion (P106/T107) [both located in the thumb] and the c-terminal extension are all in close proximity and constitute a *S.aureus* specific surface.

Please replace the paragraph beginning at **page 28, line 7**, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

Comparison of the *E.coli* and *S.aureus* crystal structures indicates that six residues in the region of the active site are conserved. In fact, five are always conserved in pdf sequences (ETB, data not shown). The residues come from the three regions of greatest sequence identity; Gxglaa (SEQ ID NO:9), EGCI (SEQ ID NO:10), and IxxqHexdhl (SEQ ID NO:11), where the capitalization indicates a conserved residue in the active site crevice. The first glycine is the lone invariant amino acid on the right side of the cleft (Figure 15). The glutamic-glycine-cysteine triplet forms the invariant left side of the crevice. Finally, isoleucine and histidine are found at the bottom of the active site crevice (Figure 15). These conserved residues form a continuous invariant surface which extends from the methionine (caproyl) site (S1) and up the left wall of the crevice. The variable residues encircle the upper aspect of the crevice. The differences account for the subtle differences in crevice shape when the two enzymes are compared---and presumably will be important determinates for inhibitor specificity.

Please replace the paragraph beginning at **page 65, line 5**, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

#### SEQUENCE LISTING FREE TEXT

SEQ ID NO:1 *Staphylococcus aureus* peptide deformylase with C-terminal 6xHis tag

SEQ ID NO:2 *Escherichia coli* peptide deformylase

SEQ ID NO:3 *Haemophilis influenzae* peptide deformylase

SEQ ID NO:4 *Bacillus subtilis* peptide deformylase

SEQ ID NO:5 *Mycoplasma pneumoniae* peptide deformylase

SEQ ID NO:6 *Staphylococcus aureus* def1 gene (Pseudo pdf)

SEQ ID NO:7 *Staphylococcus aureus* peptide deformylase

**Preliminary Amendment**

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For: CRYSTALLIZATION AND STRUCTURE OF *STAPHYLOCOCCUS AUREUS* PEPTIDE DEFORMYLASE

SEQ ID NO:8 *Escherichia coli* peptide deformylase

SEQ ID NO:9 Amino Acid Residue

SEQ ID NO:10 Amino Acid Residue

SEQ ID NO:11 Amino Acid Residue